

## SEQUENCE LISTING

<110> Conklin, Darrell C.  
 Yamamoto, Gayle  
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<120> BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOG,  
 ZNSSP6

<130> 98-80

<150> 60/115,721

<151> 1999-01-12

<160> 19

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1420

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (135)...(1271)

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tccagctgcc gttc atg ctt cct ccc cag cct tcc gca gcc cac cag gga	170
Met Leu Pro Pro Gln Pro Ser Ala Ala His Gln Gly	
1 5 10	
agg ggc ggt agg agt ggc ctt tta cca aag gga ccg gcg atg ctc tgc	218
Arg Gly Gly Arg Ser Gly Leu Leu Pro Lys Gly Pro Ala Met Leu Cys	
15 20 25	
agg ctg tgc tgg ctg gtc tcg tac agc ttg gct gtg ctg ttg ctc ggc	266
Arg Leu Cys Trp Leu Val Ser Tyr Ser Leu Ala Val Leu Leu Leu Gly	
30 35 40	

tgc Cys 45	ctg Leu	ctc Leu	ttc Phe	ctg Leu	agg Arg 50	aag Lys	gcg Ala	gcc Ala	aag Lys	ccc Pro 55	gca Ala	gga Gly	gac Asp	ccc Pro	acg Thr 60	314
gcc Ala	cac His	cag Gln	cct Pro	ttc Phe 65	tgg Trp	gct Ala	ccc Pro	cca Pro	aca Thr 70	ccc Pro	cgt Arg	cac His	agc Ser	cgg Arg 75	tgt Cys	362
cca Pro	ccc Pro	aac Asn	cac His 80	aca Thr	gtg Val	tct Ser	agc Ser	gcc Ala 85	tct Ser	ctg Leu	tcc Ser	ctg Leu	cct Pro 90	agc Ser	cgt Arg	410
cac His	cgt Arg	ctc Leu 95	ttc Phe	ttg Leu	acc Thr	tat Tyr	cgt Arg 100	cac His	tgc Cys	cga Arg	aat Asn	ttc Phe 105	tct Ser	atc Ile	ttg Leu	458
ctg Leu 110	gag Glu	cct Pro	tca Ser	ggc Gly	tgt Cys 115	tcc Ser	aag Lys	gat Asp	acc Thr	ttc Phe	ttg Leu 120	ctc Leu	ctg Leu	gcc Ala	atc Ile	506
aag Lys 125	tca Ser	cag Gln	cct Pro	ggc Gly	cac His 130	gtg Val	gag Glu	cga Arg	cgt Arg	gcg Ala 135	gct Ala	atc Ile	cgc Arg	agc Ser	acg Thr 140	554
tgg Trp	ggc Gly	agg Arg	gtg Val	ggg Gly 145	gga Gly	tgg Trp	gct Ala	agg Arg	ggc Gly 150	cgg Arg	cag Gln	ctg Leu	aag Lys	ctg Leu 155	gtg Val	602
ttc Phe	ctc Leu	cta Leu	ggg Gly 160	gtg Val	gca Ala	gga Gly	tcc Ser	gct Ala 165	ccc Pro	cca Pro	gcc Ala	cag Gln	ctg Leu 170	ctg Leu	gcc Ala	650
tat Tyr	gag Glu	agt Ser 175	agg Arg	gag Glu	ttt Phe	gat Asp	gac Asp 180	atc Ile	ctc Leu	cag Gln	tgg Trp	gac Asp 185	ttc Phe	act Thr	gag Glu	698
gac Asp 190	ttc Phe	ttc Phe	aac Asn	ctg Leu	acg Thr	ctc Leu 195	aag Lys	gag Glu	ctg Leu	cac His	ctg Leu 200	cag Gln	cgc Arg	tgg Trp	gtg Val	746
gtg Val 205	gct Ala	gcc Ala	tgc Cys	ccc Pro	cag Gln 210	gcc Ala	cat His	ttc Phe	atg Met	cta Leu 215	aag Lys	gga Gly	gat Asp	gac Asp	gat Asp 220	794

gtc ttt gtc cac gtc ccc aac gtg tta gag ttc ctg gat ggc tgg gac 842  
 Val Phe Val His Val Pro Asn Val Leu Glu Phe Leu Asp Gly Trp Asp  
 225 230 235

cca gcc cag gac ctc ctg gtg gga gat gtc atc cgc caa gcc ctg ccc 890  
 Pro Ala Gln Asp Leu Leu Val Gly Asp Val Ile Arg Gln Ala Leu Pro  
 240 245 250

aac agg aac act aag gtc aaa tac ttc atc cca ccc tca atg tac agg 938  
 Asn Arg Asn Thr Lys Val Lys Tyr Phe Ile Pro Pro Ser Met Tyr Arg  
 255 260 265

gcc acc cac tac cca ccc tat gct ggt ggg gga gga tat gtc atg tcc 986  
 Ala Thr His Tyr Pro Pro Tyr Ala Gly Gly Gly Tyr Val Met Ser  
 270 275 280

aga gcc aca gtg cgg cgc ctc cag gct atc atg gaa gat gct gaa ctc 1034  
 Arg Ala Thr Val Arg Arg Leu Gln Ala Ile Met Glu Asp Ala Glu Leu  
 285 290 295 300

ctc tcc att gat gat gtc ttt gtg ggt atg tgc ctg agg agg ctg ggg 1082  
 Leu Ser Ile Asp Asp Val Phe Val Gly Met Cys Leu Arg Arg Leu Gly  
 305 310 315

ctg agc cct atg cac cat gct ggc ttc aag aca ttt gga atc cgg cgg 1130  
 Leu Ser Pro Met His His Ala Gly Phe Lys Thr Phe Gly Ile Arg Arg  
 320 325 330

ccc ctg gac ccc tta gac ccc tgc ctg tat agg ggg ctc ctg ctg gtt 1178  
 Pro Leu Asp Pro Leu Asp Pro Cys Leu Tyr Arg Gly Leu Leu Leu Val  
 335 340 345

cac cgc ctc agc ccc ctc gag atg tgg acc atg tgg gca ctg gtg aca 1226  
 His Arg Leu Ser Pro Leu Glu Met Trp Thr Met Trp Ala Leu Val Thr  
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gat gag ggg ctc aag tgt gca gct ggc ccc ata ccc cag cgc tga 1271  
 Asp Glu Gly Leu Lys Cys Ala Ala Gly Pro Ile Pro Gln Arg \*  
 365 370 375

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<213> Homo sapiens

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			20					25					30		
Leu	Val	Ser	Tyr	Ser	Leu	Ala	Val	Leu	Leu	Leu	Gly	Cys	Leu	Leu	Phe
		35				40						45			
Leu	Arg	Lys	Ala	Ala	Lys	Pro	Ala	Gly	Asp	Pro	Thr	Ala	His	Gln	Pro
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Phe	Trp	Ala	Pro	Pro	Thr	Pro	Arg	His	Ser	Arg	Cys	Pro	Pro	Asn	His
65					70					75					80
Thr	Val	Ser	Ser	Ala	Ser	Leu	Ser	Leu	Pro	Ser	Arg	His	Arg	Leu	Phe
				85					90					95	
Leu	Thr	Tyr	Arg	His	Cys	Arg	Asn	Phe	Ser	Ile	Leu	Leu	Glu	Pro	Ser
			100					105					110		
Gly	Cys	Ser	Lys	Asp	Thr	Phe	Leu	Leu	Leu	Ala	Ile	Lys	Ser	Gln	Pro
		115				120						125			
Gly	His	Val	Glu	Arg	Arg	Ala	Ala	Ile	Arg	Ser	Thr	Trp	Gly	Arg	Val
	130					135					140				
Gly	Gly	Trp	Ala	Arg	Gly	Arg	Gln	Leu	Lys	Leu	Val	Phe	Leu	Leu	Gly
145					150					155					160
Val	Ala	Gly	Ser	Ala	Pro	Pro	Ala	Gln	Leu	Leu	Ala	Tyr	Glu	Ser	Arg
				165					170					175	
Glu	Phe	Asp	Asp	Ile	Leu	Gln	Trp	Asp	Phe	Thr	Glu	Asp	Phe	Phe	Asn
			180					185					190		
Leu	Thr	Leu	Lys	Glu	Leu	His	Leu	Gln	Arg	Trp	Val	Val	Ala	Ala	Cys
		195					200					205			
Pro	Gln	Ala	His	Phe	Met	Leu	Lys	Gly	Asp	Asp	Asp	Val	Phe	Val	His
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Val	Pro	Asn	Val	Leu	Glu	Phe	Leu	Asp	Gly	Trp	Asp	Pro	Ala	Gln	Asp
225					230					235					240
Leu	Leu	Val	Gly	Asp	Val	Ile	Arg	Gln	Ala	Leu	Pro	Asn	Arg	Asn	Thr
				245				250						255	
Lys	Val	Lys	Tyr	Phe	Ile	Pro	Pro	Ser	Met	Tyr	Arg	Ala	Thr	His	Tyr
			260					265					270		
Pro	Pro	Tyr	Ala	Gly	Gly	Gly	Gly	Tyr	Val	Met	Ser	Arg	Ala	Thr	Val
		275					280					285			
Arg	Arg	Leu	Gln	Ala	Ile	Met	Glu	Asp	Ala	Glu	Leu	Leu	Ser	Ile	Asp
	290					295				300					
Asp	Val	Phe	Val	Gly	Met	Cys	Leu	Arg	Arg	Leu	Gly	Leu	Ser	Pro	Met
305					310					315					320

His His Ala Gly Phe Lys Thr Phe Gly Ile Arg Arg Pro Leu Asp Pro  
                           325                          330                          335  
 Leu Asp Pro Cys Leu Tyr Arg Gly Leu Leu Leu Val His Arg Leu Ser  
                           340                          345                          350  
 Pro Leu Glu Met Trp Thr Met Trp Ala Leu Val Thr Asp Glu Gly Leu  
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 Lys Cys Ala Ala Gly Pro Ile Pro Gln Arg  
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 <213> Artificial Sequence

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 <223> degenerate sequence

<221> variation  
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 <223> n is any nucleotide

<221> misc\_feature  
 <222> (1)...(1134)  
 <223> n = A,T,C or G

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ytnytnytn	gntggytnt	nttytnmgn	aargcngcna	arccngcngg	ngayccnacb	180
gncaycarc	cnttytgggc	nccnccnacb	ccnmgncaym	snmgntgycc	nccnaaycay	240
acngtnwsnw	sngcnwsnyt	nwsnytnccn	wsnmgncaym	gnytnnttyt	nacntaymgn	300
caytgymgna	ayttywsnat	hytnytngr	ccnwsnggnt	gywsnaarga	yacnttyytn	360
ytnytnngcna	thaarwsnca	rccnggncay	gtngarmgmn	gngcngcnat	hmgwnsnacb	420
tggggnmgng	tnggnggntg	ggcnmgnggn	mgncarytna	arytngtntt	yytnytnngn	480
gtngcnggnw	sngcncncc	ngcncarytn	ytngcntayg	arwsnmgnga	rttygaygay	540
athytncart	gggayttyac	ngargaytty	tyaayytna	cnytnaarga	rytncaaytn	600
carmgntggg	tngtnngcng	ntgyccncar	gncayttya	tgytnaargg	ngaygaygay	660
gtnttygtnc	aygtncnaa	ygtnytngr	tyytngayg	gntgggaycc	ngcncargay	720
ytnytngtng	gngaygtnat	hmgncargcn	ytncnaaym	gnaayacnaa	rgtnaartay	780
tyathccnc	cnwsnatgta	ymgngcnaen	caytayccnc	cntaygcngg	nggnggnggn	840
taygtnatgw	snmgngcnac	ngtnmgngmn	ytncargcna	thatggarga	ygcngarytn	900
ytnwsnathg	aygaygtntt	ygtnggnatg	tgyytnmgmn	gnytnngnyt	nwsnccnatg	960
caycaygcng	gnttyaarac	nttygggnath	mgnmgnccny	tngayccny	ngayccntgy	1020
ytnaymgng	gnytnytny	ngtncaymgn	ytnwsnccny	tngaratgtg	gacnatgtg	1080
gcnytngtna	cngaygargg	nytnaartgy	gcngcnggnc	cnathccnca	rmgn	1134

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 <223> oligonucleotide primer

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 ccacctaata acgactcact atagggc

27

<210> 5  
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23

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<400> 6  
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23

<210> 7  
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<400> 7  
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23

<210> 8  
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<400> 9

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24

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<400> 12  
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 <212> DNA  
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 <212> DNA  
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<210> 17  
 <211> 65  
 <212> DNA  
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<220>  
 <223> Oligonucleotide primer

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 <211> 65  
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<210> 19  
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<400> 19

60  
120